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TECH CENTER 1600/2900

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/913,329

DATE: 12/10/2001

TIME: 15:24:43

Input Set : A:\ES.txt

Output Set: N:\CRF3\12102001\I913329.raw

ENTERED

3 <110> APPLICANT: UNIVERSITE DE MONTREAL  
 5 <120> TITLE OF INVENTION: NEW METALLOPROTEASES OF THE NEPRILYSIN FAMILY  
 7 <130> FILE REFERENCE: BIOMEIP INC. NEPRILYSIN  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/913,329  
 C--> 10 <141> CURRENT FILING DATE: 2001-12-10  
 12 <150> PRIOR APPLICATION NUMBER: 2,260,376  
 13 <151> PRIOR FILING DATE: 1999-02-11  
 15 <160> NUMBER OF SEQ ID NOS: 17  
 17 <170> SOFTWARE: PatentIn Ver. 2.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 750  
 21 <212> TYPE: PRT  
 22 <213> ORGANISM: Homo sapiens  
 24 <400> SEQUENCE: 1  
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 26 1 5 10 15  
 28 Lys Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser  
 29 20 25 30  
 31 Val Leu Val Leu Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu  
 32 35 40 45  
 34 Tyr Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys  
 35 50 55 60  
 37 Ser Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys  
 38 65 70 75 80  
 40 Thr Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val  
 41 85 90 95  
 43 Ile Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp  
 44 100 105 110  
 46 Glu Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu  
 47 115 120 125  
 49 Asp Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile  
 50 130 135 140  
 52 Asn Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu  
 53 145 150 155 160  
 55 Leu Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln  
 56 165 170 175  
 58 Lys Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn  
 59 180 185 190  
 61 Ser Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp  
 62 195 200 205  
 64 Asp Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu  
 65 210 215 220  
 67 Gly Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu  
 68 225 230 235 240  
 70 Ala Cys Thr Ala Tyr Val Asp Phe Met Ile Ser Val Ala Arg Leu Ile  
 71 245 250 255  
 73 Arg Gln Glu Glu Arg Leu Pro Ile Asp Glu Asn Gln Leu Ala Leu Glu

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```

74          260          265          270
76 Met Asn Lys Val Met Glu Leu Glu Lys Glu Ile Ala Asn Ala Thr Ala
77          275          280          285
79 Lys Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys Met Thr
80          290          295          300
82 Leu Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly Lys Pro
83 305          310          315          320
85 Phe Ser Trp Leu Asn Phe Thr Asn Glu Ile Met Ser Thr Val Asn Ile
86          325          330          335
88 Ser Ile Thr Asn Glu Glu Asp Val Val Val Tyr Ala Pro Glu Tyr Leu
89          340          345          350
91 Thr Lys Leu Lys Pro Ile Leu Thr Lys Tyr Ser Ala Arg Asp Leu Gln
92          355          360          365
94 Asn Leu Met Ser Trp Arg Phe Ile Met Asp Leu Val Ser Ser Leu Ser
95          370          375          380
97 Arg Thr Tyr Lys Glu Ser Arg Asn Ala Phe Arg Lys Ala Leu Tyr Gly
98 385          390          395          400
100 Thr Thr Ser Glu Thr Ala Thr Trp Arg Arg Cys Ala Asn Tyr Val Asn
101          405          410          415
103 Gly Asn Met Glu Asn Ala Val Gly Arg Leu Tyr Val Glu Ala Ala Phe
104          420          425          430
106 Ala Gly Glu Ser Lys His Val Val Glu Asp Leu Ile Ala Gln Ile Arg
107          435          440          445
109 Glu Val Phe Ile Gln Thr Leu Asp Asp Leu Thr Trp Met Asp Ala Glu
110          450          455          460
112 Thr Lys Lys Arg Ala Glu Glu Lys Ala Leu Ala Ile Lys Glu Arg Ile
113 465          470          475          480
115 Gly Tyr Pro Asp Asp Ile Val Ser Asn Asp Asn Lys Leu Asn Asn Glu
116          485          490          495
118 Tyr Leu Glu Leu Asn Tyr Lys Glu Asp Glu Tyr Phe Glu Asn Ile Ile
119          500          505          510
121 Gln Asn Leu Lys Phe Ser Gln Ser Lys Gln Leu Lys Lys Leu Arg Glu
122          515          520          525
124 Lys Val Asp Lys Asp Glu Trp Ile Ser Gly Ala Ala Val Val Asn Ala
125          530          535          540
127 Phe Tyr Ser Ser Gly Arg Asn Gln Ile Val Phe Pro Ala Gly Ile Leu
128 545          550          555          560
130 Gln Pro Pro Phe Phe Ser Ala Gln Gln Ser Asn Ser Leu Asn Tyr Gly
131          565          570          575
133 Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe Asp Asp
134          580          585          590
136 Asn Gly Arg Asn Phe Asn Lys Asp Gly Asp Leu Val Asp Trp Trp Thr
137          595          600          605
139 Gln Gln Ser Ala Ser Asn Phe Lys Glu Gln Ser Gln Cys Met Val Tyr
140          610          615          620
142 Gln Tyr Gly Asn Phe Ser Trp Asp Leu Ala Gly Gly Gln His Leu Asn
143 625          630          635          640
145 Gly Ile Asn Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Gly
146          645          650          655

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```

148 Gln Ala Tyr Arg Ala Tyr Gln Asn Tyr Ile Lys Lys Asn Gly Glu Glu
149          660          665          670
151 Lys Leu Leu Pro Gly Leu Asp Leu Asn His Lys Gln Leu Phe Phe Leu
152          675          680          685
154 Asn Phe Ala Gln Val Trp Cys Gly Thr Tyr Arg Pro Glu Tyr Ala Val
155          690          695          700
157 Asn Ser Ile Lys Thr Asp Val His Ser Pro Gly Asn Phe Arg Ile Ile
158 705          710          715          720
160 Gly Thr Leu Gln Asn Ser Ala Glu Phe Ser Glu Ala Phe His Cys Arg
161          725          730          735
163 Lys Asn Ser Tyr Met Asn Pro Glu Lys Lys Cys Arg Val Trp
164          740          745          750
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 749
169 <212> TYPE: PRT
170 <213> ORGANISM: Homo sapiens
172 <400> SEQUENCE: 2
173 Met Glu Ala Glu Thr Gly Ser Ser Val Glu Thr Gly Lys Lys Ala Asn
174 1          5          10          15
176 Arg Gly Thr Arg Ile Ala Leu Val Val Phe Val Gly Gly Thr Leu Val
177          20          25          30
179 Leu Gly Thr Ile Leu Phe Leu Val Ser Gln Gly Leu Leu Ser Leu Gln
180          35          40          45
182 Ala Lys Gln Glu Tyr Cys Leu Lys Pro Glu Cys Ile Glu Ala Ala Ala
183          50          55          60
185 Ala Ile Leu Ser Lys Val Asn Leu Ser Val Asp Pro Cys Asp Asn Phe
186 65          70          75          80
188 Phe Arg Phe Ala Cys Asp Gly Trp Ile Ser Asn Asn Pro Ile Pro Glu
189          85          90          95
191 Asp Met Pro Ser Tyr Gly Val Tyr Pro Trp Leu Arg His Asn Val Asp
192          100          105          110
194 Leu Lys Leu Lys Glu Leu Leu Glu Lys Ser Ile Ser Arg Arg Arg Asp
195          115          120          125
197 Thr Glu Ala Ile Gln Lys Ala Lys Ile Leu Tyr Ser Ser Cys Met Asn
198          130          135          140
200 Glu Lys Ala Ile Glu Lys Ala Asp Ala Lys Pro Leu Leu His Ile Leu
201 145          150          155          160
203 Arg His Ser Pro Phe Arg Trp Pro Val Leu Glu Ser Asn Ile Gly Pro
204          165          170          175
206 Glu Gly Val Trp Ser Glu Arg Lys Phe Ser Leu Leu Gln Thr Leu Ala
207          180          185          190
209 Thr Phe Arg Gly Gln Tyr Ser Asn Ser Val Phe Ile Arg Leu Tyr Val
210          195          200          205
212 Ser Pro Asp Asp Lys Ala Ser Asn Glu His Ile Leu Lys Leu Asp Gln
213          210          215          220
215 Ala Thr Leu Ser Leu Ala Val Arg Glu Asp Tyr Leu Asp Asn Ser Thr
216 225          230          235          240
218 Glu Ala Lys Ser Tyr Arg Asp Ala Leu Tyr Lys Phe Met Val Asp Thr
219          245          250          255

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```

221 Ala Val Leu Leu Gly Ala Asn Ser Ser Arg Ala Glu His Asp Met Lys
222      260      265      270
224 Ser Val Leu Arg Leu Glu Ile Lys Ile Ala Glu Ile Met Ile Pro His
225      275      280      285
227 Glu Asn Arg Thr Ser Glu Ala Met Tyr Asn Lys Met Asn Ile Ser Glu
228      290      295      300
230 Leu Ser Ala Met Ile Pro Gln Phe Asp Trp Leu Gly Tyr Ile Lys Lys
231 305      310      315      320
233 Val Ile Asp Thr Arg Leu Tyr Pro His Leu Lys Asp Ile Ser Pro Ser
234      325      330      335
236 Glu Asn Val Val Val Arg Val Pro Gln Tyr Phe Lys Asp Leu Phe Arg
237      340      345      350
239 Ile Leu Gly Ser Glu Arg Lys Lys Thr Ile Ala Asn Tyr Leu Val Trp
240      355      360      365
242 Arg Met Val Tyr Ser Arg Ile Pro Asn Leu Ser Arg Arg Phe Gln Tyr
243      370      375      380
245 Arg Trp Leu Glu Phe Ser Arg Val Ile Gln Gly Thr Thr Thr Leu Leu
246 385      390      395      400
248 Pro Gln Trp Asp Lys Cys Val Asn Phe Ile Glu Ser Ala Leu Pro Tyr
249      405      410      415
251 Val Val Gly Lys Met Phe Val Asp Val Tyr Phe Gln Glu Asp Lys Lys
252      420      425      430
254 Glu Met Met Glu Glu Leu Val Glu Gly Val Arg Trp Ala Phe Ile Asp
255      435      440      445
257 Met Leu Glu Lys Glu Asn Glu Trp Met Asp Ala Gly Thr Lys Arg Lys
258      450      455      460
260 Ala Lys Glu Lys Ala Arg Ala Val Leu Ala Lys Val Gly Tyr Pro Glu
261 465      470      475      480
263 Phe Ile Met Asn Asp Thr His Val Asn Glu Asp Leu Lys Ala Ile Lys
264      485      490      495
266 Phe Ser Glu Ala Asp Tyr Phe Gly Asn Val Leu Gln Thr Arg Lys Tyr
267      500      505      510
269 Leu Ala Gln Ser Asp Phe Phe Trp Leu Arg Lys Ala Val Pro Lys Thr
270      515      520      525
272 Glu Trp Phe Thr Asn Pro Thr Thr Val Asn Ala Phe Tyr Ser Ala Ser
273      530      535      540
275 Thr Asn Gln Ile Arg Phe Pro Ala Gly Glu Leu Gln Lys Pro Phe Phe
276 545      550      555      560
278 Trp Gly Thr Glu Tyr Pro Arg Ser Leu Ser Tyr Gly Ala Ile Gly Val
279      565      570      575
281 Ile Val Gly His Glu Phe Thr His Gly Phe Asp Asn Asn Gly Arg Lys
282      580      585      590
284 Tyr Asp Lys Asn Gly Asn Leu Asp Pro Trp Trp Ser Thr Glu Ser Glu
285      595      600      605
287 Glu Lys Phe Lys Glu Lys Thr Lys Cys Met Ile Asn Gln Tyr Ser Asn
288      610      615      620
290 Tyr Tyr Trp Lys Lys Ala Gly Leu Asn Val Lys Gly Lys Arg Thr Leu
291 625      630      635      640
293 Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Arg Glu Ala Phe Arg Ala

```

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TIME: 15:24:43

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```

294          645          650          655
296 Tyr Arg Lys Trp Ile Asn Asp Arg Arg Gln Gly Leu Glu Glu Pro Leu
297          660          665          670
299 Leu Pro Gly Ile Thr Phe Thr Asn Asn Gln Leu Phe Phe Leu Ser Tyr
300          675          680          685
302 Ala His Val Arg Cys Asn Ser Tyr Arg Pro Glu Ala Ala Arg Glu Gln
303          690          695          700
305 Val Gln Ile Gly Ala His Ser Pro Pro Gln Phe Arg Val Asn Gly Ala
306 705          710          715          720
308 Ile Ser Asn Phe Glu Glu Phe Gln Lys Ala Phe Asn Cys Pro Pro Asn
309          725          730          735
311 Ser Thr Met Asn Arg Gly Met Asp Ser Cys Arg Leu Trp
312          740          745
315 <210> SEQ ID NO: 3
316 <211> LENGTH: 732
317 <212> TYPE: PRT
318 <213> ORGANISM: Homo sapiens
320 <400> SEQUENCE: 3
321 Met Glu Gly Gly Asp Gln Ser Glu Glu Glu Pro Arg Glu Arg Ser Gln
322 1          5          10          15
324 Ala Gly Gly Met Gly Thr Leu Trp Ser Gln Glu Ser Thr Pro Glu Glu
325          20          25          30
327 Arg Leu Pro Val Glu Gly Ser Arg Pro Trp Ala Val Ala Arg Arg Val
328          35          40          45
330 Leu Thr Ala Ile Leu Ile Leu Gly Leu Leu Leu Cys Phe Ser Val Leu
331          50          55          60
333 Leu Phe Tyr Asn Phe Gln Asn Cys Gly Pro Arg Pro Cys Glu Thr Ser
334 65          70          75          80
336 Val Cys Leu Asp Leu Arg Asp His Tyr Leu Ala Ser Gly Asn Thr Ser
337          85          90          95
339 Val Ala Pro Cys Thr Asp Phe Phe Ser Phe Ala Cys Gly Arg Ala Lys
340          100          105          110
342 Glu Thr Asn Asn Ser Phe Gln Glu Leu Ala Thr Lys Asn Lys Asn Arg
343          115          120          125
345 Leu Arg Arg Ile Leu Glu Val Gln Asn Ser Trp His Pro Gly Ser Gly
346          130          135          140
348 Glu Glu Lys Ala Phe Gln Phe Tyr Asn Ser Cys Met Asp Thr Leu Ala
349 145          150          155          160
351 Ile Glu Ala Ala Gly Thr Gly Pro Leu Arg Gln Val Ile Glu Glu Leu
352          165          170          175
354 Gly Gly Trp Arg Ile Ser Gly Lys Trp Thr Ser Leu Asn Phe Asn Arg
355          180          185          190
357 Thr Leu Arg Leu Leu Met Ser Gln Tyr Gly His Phe Pro Phe Phe Arg
358          195          200          205
360 Ala Tyr Leu Gly Pro His Pro Ala Ser Pro His Thr Pro Val Ile Gln
361          210          215          220
363 Ile Asp Gln Pro Glu Phe Asp Val Pro Leu Lys Gln Asp Gln Glu Gln
364 225          230          235          240
366 Lys Ile Tyr Ala Gln Ile Phe Arg Glu Tyr Leu Thr Tyr Leu Asn Gln

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/913,329

DATE: 12/10/2001

TIME: 15:24:44

Input Set : A:\ES.txt

Output Set: N:\CRF3\12102001\I913329.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11